

*CRIS*  
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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 7/10/06  
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/765,456  
Location (Bldg/Room#): Roman 2A79 (Mailbox #): 2C70 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

Search Topic:

*Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.*

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular plus interference sequence search on SEQ ID NO: 1 and 3.

seq 1 - 521AA  
seq 3 - 1584NA

*Thanks*

RECEIVED  
JUL 10 2006  
USPTO/CHEM. DIVISION  
(SITC)

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: July 11, 2006, 08:30:11 ; Search time 41 Seconds

(without alignments)  
1236.737 Million cell updates/sec

Title: US-10-765-456-1

Perfect score: 2790

Sequence: 1 MNQTSKNDSDLVLODEM**GOKT**FESERKSLSLGSIGRPHFSRGIELREVKA 527

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	244.5	8.8	710	2 T50469	hypothetical protein
2	244.5	8.8	710	2 A25657	hypothetical protein
3	244.5	8.8	720	2 T50475	hypothetical protein
4	213	7.6	470	2 E97331	reverse transcript
5	205.5	7.4	418	2 H83677	transposase (11) B
6	204.5	7.3	418	2 G83654	transposase (11) B
7	178.5	6.4	599	2 S77648	maturase-related p
8	171.5	6.1	453	2 A95946	probable reverse t
9	166.5	6.0	790	2 E8327	COI intron A prote
10	163.5	5.9	392	2 G96004	probable reverse t
11	161	5.8	574	2 T0245	reverse transcript
12	157	5.6	788	2 B48327	COI intron alpha-s
13	156.5	5.5	318	2 S58503	reverse transcript
14	155	5.6	602	2 G59091	hypothetical protein
15	154	5.5	461	2 G59093	hypothetical protein
16	154	5.5	668	2 G96029	hypothetical protein
17	154	5.5	1260	4 GNLRL1	reverse transcript
18	153	5.5	368	2 S01651	probable RNA-direc
19	151	5.4	633	2 T31160	maturase-related p
20	148.5	5.3	1084	2 T1160	RNA-directed DNA p
21	146.5	5.3	608	2 S05341	probable reverse t
22	146	5.2	308	2 S58504	reverse transcript
23	144	5.2	785	2 S63652	hypothetical prote
24	141	5.1	834	1 QXBY31	gene coxi intron 1
25	141	5.1	834	2 S78642	hypothetical gene coxi intron 1
26	138.5	5.0	416	2 S5028	hypothetical prote
27	137	4.9	1352	2 G84473	transposase, uncha
28	136	4.9	330	2 E98119	RNA-directed DNA p
29	136	4.9	860	2 S55543	

## ALIGNMENTS

RESULT 1  
T50469  
hypothetical protein [imported] - Neurospora crassa mitochondrial plasmid Varkud  
C.Species: mitochondrial Neurospora crassa  
C.Date: 9-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C.Accession: T50469  
R.Akins, R.A., Grant, D.M.; Stohl, L.L.; Bottorff, D.A.; Nargang, F.E.; Lambowitz, A.M.  
J. Mol. Biol. 204, 1-25, 1988  
A.Title: Nucleotide sequence of the Varkud mitochondrial plasmid of Neurospora and synt  
A.Reference number: Z225078; MUID:89110991; PMID:3216387  
A.Accession: 150469  
A.Status: preliminary; translated from GB/EMBL/DBTC  
A.Molecule type: DNA  
A.Residues: 1-710 <AA>  
A>Cross-references: UNIPROT:Q35156; UNIPARC:UPI00000925AS; EMBL:X13801; NID:92941; PIDA  
A;Genetics: C;Genetic code: SGC3  
A;Introns: 30/3  
C;Keywords: mitochondrion

Query Match 8.8%; Score 244.5; DB 2; Length 710;  
Best Local Similarity 25.4%; Pred. No. 2.4e-09;  
Matches 95; Conservative 51; Mismatches 151; Indels 67; Gaps 13;

QY 1 MNQTSKNDSDLVLODEM**GOKT**FESERKSLSLGSIGRPHFSRGIELREVKA 60  
Db 10 VSVLGENHNLWSLWKGMPFLKRSNPSQTGGMLW-----LNHG-----P 47

QY 61 NRVLAQFQEORIVSAEAGSEIRKAVLWGLMKVRSVQILLFRVCKGSIWSTARVE 120  
Db 48 NGFVKYMMILMGHARDKQDAKEYWRIGSLMK-NEAFQVOAFNVCQHQLDKRPHIAK 106

QY 121 IIGGMANNKRSWPMKLLIHRPFYLLKNGKSRPPIGAQNYESRMTSKALTDL--YSITKS 178  
Db 107 LLKEVRENEVELQPVICDIDKRVVLPKAMQKQRPLGIVPYPTWPRVYLHMVNVLLWVRIQPQD 166

QY 179 RSAEOHGMKMKRGWSATLLECHSKLKGAGYBFDKSFFENTVEPTYFRKLI--VUKK 236  
Db 167 --NOHANFPKRKGVTAWRALWPKL-DSQNTIEFDLKKNFFPSVDAYLKDKLUMESGIPQD 222

QY 237 LTKLISNYNTKGLEYRFEE-LIPE-----SELNPKANRKTLE----- 272  
Db 223 ISBYLTWLNLSLVLTSEDKIPEPHRDVFINSDTGNPDNPNLKPDQCRILKOPDPFVEILRR 282

QY 273 -----RTGVPOGLSLSPPLSTWAL-EYCPRENIMMADGIVFFKHNITSKFTWIER 324  
Db 283 RGFTDIATNGPQGASTSGIATYNNKELPFRYDELIMYADDGI-LCRQDPSTPPRSIE- 340

Oy 325 MGRAGIBISPEKSG 338  
Db 341 --EASYVQEPAKSG 352

Scoring table:						
BLOSUM62						
Gapop 10.0 , Gapext 0.5						
Searched:	2849598 seqs, 925015592 residues					
Total number of hits satisfying chosen parameters:	2849598					
Minimum DB seq length: 0						
Maximum DB seq length: 200000000						
Post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	UniProt_7.2:*					
	1: uniprot_sprot:*					
	2: uniprot_trembl:*					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	ALIGNMENTS
1	2790	100.0	527	2	Q9XNK5_FUSOX	RESULT 1
2	2550	91.4	527	2	Q9XNK4_FUSOX	ID Q9XNK5_FUSOX PRELIMINARY; PRT; 527 AA.
3	2052	53.5	397	2	Q9XN5; fusarium ox	AC Q9XNK5; 01-NOV-1999, integrated into UniProtKB/Trembl.
4	420	15.1	262	2	Q21165_FUSOX	DT 01-NOV-1999, sequence version 1.
5	315	11.3	605	2	Q9XN5; fusarium ox	DT 07-FEB-2006, entry version 23.
6	270.5	9.7	294	Q9XNG3_EPTYA	DE Reverse transcriptase.	
7	245.5	8.8	710	2	Q9XNG1_NEUIN	DS Fusarium oxysporum f. sp. raphani.
8	244.5	8.8	710	2	Q9XNG0_NEUIN	OG Mitochondrion.
9	244.5	8.8	710	2	Q7GEY3_NEUCR	OC Plasmid PROK22.
10	244.5	8.8	720	2	Q35156_NEUIN	OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Fusarium; Fusarium oxysporum complex.
11	243.5	8.7	710	Q35158_NEUCC	OC NCBI_TAXID=96318; RN [1];	
12	227.5	8.2	439	2	Q3C244_STRA8	RP NUCLEOTIDE SEQUENCE.
13	227.5	8.2	439	2	Q8E028_STRA5	RC STRAIN=699; PubMed=10488338; DOI=10.1016/S1097-2765(00)80370-6;
14	220	7.9	482	Q3GD88_SFIRN	RX MEDLINE=99417962; PubMed=10488338; DOI=10.1016/S1097-2765(00)80370-6;	
15	219.5	7.9	433	2	Q2WLQ7_CLOBE	RA Walther T.C., Kennell J.C.;
16	216.5	7.8	470	2	Q3CKT1_THEBT	RT "Linear mitochondrial plasmids of <i>F. oxysporum</i> are novel, telomere-like retroelements.";
17	214.5	7.7	470	2	Q3CKT2_THEBT	RT Mol. Cell 4:229-338 (1999).
18	214	7.7	462	2	Q3CKT4_NSPHI	RT --! SIMILARITY: Contains 1 reverse transcriptase domain.
19	213.5	7.7	470	2	Q3CESS_THEBT	CC 09XNK5; C-mitochondrion; IEA.
20	213	7.6	470	2	Q3CGH6_THEBT	CC Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
21	213	7.6	470	2	Q3DGJ3_CLOBR	CC Distributed under the Creative Commons Attribution-NoDerivs License
22	212	7.6	470	2	Q3CJR9_THEBT	CC EMLI; AP124843; RAD3803.1; Genomic_DNA.
23	212	7.6	470	2	Q3CJ48_THEBT	DR GO; GO:0005739; C-mitochondrion; IEA.
24	211.5	7.6	468	2	Q8A412_BACIN	DR GO; GO:0003123; F: RNA binding; IEA.
25	210.5	7.5	412	2	Q75TM9_9BACT	DR GO; GO:0003364; F: RNA-directed DNA polymerase activity; IEA.
26	210	7.5	470	2	Q3CJ12_THEBT	DR GO; GO:0006728; P: RNA-dependent DNA replication; IEA.
27	209	7.5	470	2	Q3CJ11_THEBT	DR InterPro; IPR000477; RVSE.
28	208.5	7.5	469	2	Q42Q97_DESII	DR Prosite; PP00078; RT; POL; 1.
29	207	7.4	470	2	Q3CER4_THEET	RW Mitochondrion; Plasmid; RNA-directed DNA Polymerase.
30	207	7.4	470	2	Q3CGH40_THEET	KW Query Match 100.0%; Score 2790; DB 2; Length 527;
31	207	7.4	470	2	Q3CGH0_THEET	MATCHES 527; Conservatice 100.0%; Pred. No. 7e-188; Mismatches 0; Indels 0; Gaps 0;
32	205.5	7.4	418	2	Q9KG88_BACHD	Q9KG88 bacillus ha
33	205.5	7.4	423	2	Q4JGS6_LACCRE	Q9JGS6 lactobacill
34	205.5	7.4	604	2	Q73Q33_BACCI	Q73Q33 bacillus ce
35	205	7.3	418	2	Q75TR9_BACHD	Q75TR9 bacillus ha
36	204.5	7.3	412	2	Q75TN1_BACAG	Q75TN1 bacillus ag
37	204.5	7.3	412	2	Q75TN4_BACCI	Q75TN4 bacillus cl
38	204.5	7.3	412	2	Q75TN5_BACFI	Q75TN5 bacillus fi
39	204.5	7.3	418	2	Q75TR8_BACHD	Q75TR8 bacillus ha
40	204.5	7.3	418	2	Q9WRR9_BACCI	Q9WRR9 bacillus ha
41	204	7.3	434	2	Q74AB9_GROSL	Q74AB9 geobacter s
42	203.5	7.3	418	2	Q75RN8_BACCS	Q75RN8 bacillus ha
43	202.5	7.3	418	2	Q75RN2_BACCD	Q75RN2 bacillus cl
44	202.5	7.3	418	2	Q75RS2_BACCI	Q75RS2 bacillus ce
45	198.5	7.1	627	2	Q74P60_BACCI	Q74P60 bacillus ce

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GenCore version 5.1.9

(without alignments)

1254.964 Million cell updates/sec

### Om protein - protein search, using sw model

Run on: July 11, 2006, 08:26:26 ; Search time 192 Seconds

US-10-765-456-1  
2790 seqs, 457216429 residues

Title: US-10-765-456-1

perfect score:

1 MNQISKNDSDLVLDLQDEMGOK.....YWEIMQFHNLUKQQQLRAIE 527

Scoring table: BLOSUM62

Gapov 10.0 , Gapext 0.5

Searched:

2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:

2589679

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A\_Geneseq 8.0

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003ab:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

ID ADR14865

standard; protein; 527 AA.

XX

AC

ADR14865;

XX

DT

04-NOV-2004 (first entry)

XX

DE

F. oxysporum reverse transcriptase from pFOXC2.

XX

Reverse transcriptase; RT; pFOXC2; pFOXC3; 3' mismatch; cDNA synthesis;

KW small RNA; small interfering RNA; RNA interference; gene silencing;

KW siRNA.

XX

OS Fusarium oxysporum.

XX

PN

US2004157213-A1.

XX

PD

12-AUG-2004.

XX

PP

26-JUN-2004; 2004US-00765456.

XX

PR

27-JAN-2003; 2003US-0442885P.

PR

02-APR-2003; 2003US-0459775P.

XX

PA (KENN/1) KENNELL J C.

XX

PI

Kennell JC;

XX

DR

WPI: 2004-580263/56.

DR

N-PSDB; ADR14867, ADR14869.

XX

PT

New isolated fungal reverse transcriptases with enhanced capabilities,

PR and encoding nucleic acid molecules, useful for research and diagnostic

PT applications.

XX

PS

Claim 1; SEQ ID NO 1; 35pp; English.

XX

CC

The invention relates to an isolated polynucleotide comprising a sequence

CC that encodes a reverse transcriptase polypeptide comprising a sequence having 88%<sup>1</sup>

reverse transcriptase polypeptide identity to ADR14865 or ADR14866, the reverse transcriptases encoded by

CC C. acerob

CC Aed01456

CC Abp30367

CC recombinant vector comprising a polynucleotide sequence (encoding the

CC reverse transcriptases) appearing as ADR14867-ADR14870, a cell comprising

CC an isolated polynucleotide that encodes a pFOXC-RT, making a pFOXC-RT

CC example p

Abg04464

Novel hum

Abg23203

Novel hum

Abg22665

Example p

Abg14899

Novel hum

Abg1978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg068655

Pseudomon

Abg07234

Pseudomon

Abg07135

Pseudomon

Abg01457

Pseudomon

Abg010260

Novel hum

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg068655

Pseudomon

Abg07234

Pseudomon

Abg07135

Pseudomon

Abg01457

Pseudomon

Abg010260

Novel hum

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

Pseudomon

Abg068712

Pseudomon

Abg010131

Novel hum

Abg068655

Pseudomon

Abg01978

Novel hum

Abg02186

Novel hum

Abg06712

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GenCore version 5.1.9

Run on: July 11, 2006, 08:47:17 ; Search time 185 Seconds  
 (without alignments)

Scoring table: BLOSUM62

Title: US-10-765-456-1

Perfect score: 2790

Sequence: 1 MNQISKNDSDLVQDEMOKTTESERKSLSLGSIGLPHESRCIELREVKA 527

Scoring table: Gapop 10.0 , Gapext 0.5

Searched:

2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Maximum DB seq length: 0

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

1: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us07\_PUBCOMB.pep.\*

2: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us08\_PUBCOMB.pep.\*

3: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us09\_PUBCOMB.pep.\*

4: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us10\_PUBCOMB.pep.\*

5: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us10B\_PUBCOMB.pep.\*

6: /EMC\_Celerra\_SIDS3\_ptodata/2/pubpaal/us11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1

US-10-765-456-1

Sequence 1, Application US/10765456

Publication No. US20040157213A1

GENERAL INFORMATION:

APPLICANT: Kennell, John C.

TITLE OF INVENTION: Fungal Reverse Transcriptases with Enhanced Capabilities

FILE REFERENCE: SU02-010

CURRENT APPLICATION NUMBER: US/10-765, 456

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: 601442, 885

PRIOR FILING DATE: 2003-01-27

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Microsoft Word 2000

SEQ ID NO: 1

LENGTH: 527

TYPE: PRT

ORGANISM: Fungal

US-10-765-456-1

ALIGNMENTS

SEQUENCES

SUMMARIES

RESULTS

REPORT

SEARCH

SEARCHER

</div



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OM protein - protein search, using sw model

Run on: July 11, 2006, 08:36:01 ; Search time 605 Seconds (without alignments)

Title: US-10-765-456-1

Perfect score: 2790

Sequence: 1 MNQISKNDSDLVLDQDGOK..... YWEIMGFHNLRQQLRAIE 527

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\*, Maximum Match 100\*, Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US066 COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US073 COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US074 COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US075 COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US076 COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US077 COMB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US078 COMB.pep:\*

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13: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US083 COMB.pep:\*

14: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US084 COMB.pep:\*

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16: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US086 COMB.pep:\*

17: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US087 COMB.pep:\*

18: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US088 COMB.pep:\*

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21: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US091 COMB.pep:\*

22: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US092 COMB.pep:\*

23: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US093 COMB.pep:\*

24: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US094 COMB.pep:\*

25: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US095 COMB.pep:\*

26: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US096 COMB.pep:\*

27: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US097 COMB.pep:\*

28: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US098 COMB.pep:\*

29: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US099 COMB.pep:\*

30: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US100 COMB.pep:\*

31: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US101 COMB.pep:\*

32: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US102 COMB.pep:\*

33: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US103 COMB.pep:\*

34: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US104 COMB.pep:\*

35: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US105 COMB.pep:\*

36: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US106 COMB.pep:\*

37: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US107 COMB.pep:\*

38: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US108 COMB.pep:\*

39: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US109 COMB.pep:\*

40: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US110 COMB.pep:\*

41: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US111 COMB.pep:\*

42: /EMC\_Celerra\_SIDS3/ptodata/2/paa/US112 COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query length	DB ID	Description
1	2790	100.0	527	37 US-10-765-456-1 Sequence 1, Appli
2	2550	91.4	527	37 US-10-765-456-1 Sequence 2, Appli
3	227.5	8.2	439	34 US-10-415-182A-1488 Sequence 1488, App
4	212.5	7.6	420	1 PCT-US02-36123-312 Sequence 312, App
5	212.5	7.6	420	1 PCT-US02-36123-564 Sequence 564, App
6	212.5	7.6	420	1 PCT-US02-36123-870 Sequence 870, App
7	212.5	7.6	420	1 PCT-US02-36123-4116 Sequence 4116, App
8	212.5	7.6	420	1 PCT-US02-36123-6084 Sequence 6084, App
9	212.5	7.6	420	1 PCT-US02-36123-712 Sequence 312, App
10	212.5	7.6	420	1 PCT-US02-36123-282-564 Sequence 564, App
11	212.5	7.6	420	1 PCT-US02-36123-870 Sequence 870, App
12	212.5	7.6	420	1 PCT-US02-36123-3944 Sequence 3944, App
13	212.5	7.6	420	1 PCT-US02-36123-3952 Sequence 3952, App
14	212.5	7.6	431	1 PCT-US02-36123-4118 Sequence 4118, App
15	212.5	7.6	431	1 PCT-US02-36123-556 Sequence 556, App
16	212.5	7.6	431	1 PCT-US02-36123-872 Sequence 872, App
17	212.5	7.6	431	1 PCT-US02-36123-1598 Sequence 1598, App
18	212.5	7.6	431	1 PCT-US02-36123-3944 Sequence 3944, App
19	212.5	7.6	431	1 PCT-US02-36123-3952 Sequence 3952, App
20	212.5	7.6	431	1 PCT-US02-36123-4118 Sequence 4118, App
21	212.5	7.6	431	1 PCT-US02-36123-6086 Sequence 6086, App
22	212.5	7.6	431	1 PCT-US02-36123-282-314 Sequence 314, App
23	212.5	7.6	431	1 PCT-US02-36123-501 Sequence 501, App
24	212.5	7.6	431	1 PCT-US02-36123-566 Sequence 566, App
25	212.5	7.6	431	1 PCT-US02-36123-872 Sequence 872, App
26	212.5	7.6	431	1 PCT-US02-36123-3944 Sequence 3944, App
27	212.5	7.6	431	1 PCT-US02-36123-4118 Sequence 4118, App
28	212.5	7.6	431	1 PCT-US02-36123-6086 Sequence 6086, App
29	212.5	7.6	431	1 PCT-US02-36123-872 Sequence 872, App
30	210.5	7.5	420	1 PCT-US02-36123-858 Sequence 858, App
31	210.5	7.5	420	1 PCT-US02-36123-858 Sequence 858, App
32	210.5	7.5	431	1 PCT-US02-36122-860 Sequence 860, App
33	210.5	7.5	431	1 PCT-US02-36122-860 Sequence 860, App
34	194	7.0	425	34 US-10-415-182A-990 Sequence 990, App
35	194	7.0	436	34 US-10-415-182A-6090 Sequence 6090, App
36	190.5	6.8	467	22 US-09-252-691-6535 Sequence 6535, App
37	190.5	6.8	467	22 US-09-252-691-6535 Sequence 6535, App
38	189.5	6.8	467	34 US-10-417-886-6535 Sequence 6535, App
39	189.5	6.8	628	35 US-10-550-119-224 Sequence 224, App
40	187.5	6.7	599	1 PCT-US99-04049-6 Sequence 6, Appli
41	185	6.6	599	1 PCT-US99-04049-6 Sequence 6, Appli
42	185	6.6	420	37 US-10-797-262-2 Sequence 2, Appli
43	185	6.6	455	37 US-10-797-262-2 Sequence 2, Appli
44	180	6.5	506	1 PCT-US02-09161-6129 Sequence 6129, A
45	180	6.5	506	1 PCT-US02-09161-6129 Sequence 6129, A

## ALIGNMENTS

Sequence 1732, Ap  
Sequence 2335, App  
Sequence 7999, Ap  
Sequence 4292, Ap  
Sequence 4292, Ap  
Sequence 194, Ap  
Sequence 45, App  
Sequence 268, App  
Sequence 260, App  
Sequence 15561, A  
Sequence 4038, Ap  
Sequence 4038, Ap  
Sequence 26091, A  
Sequence 188, App  
Sequence 189, App  
Sequence 9060, Ap  
Sequence 19, App  
Sequence 40, App  
Sequence 53, App

Om nucleic - nucleic search, using bw model

Run on: July 11, 2006, 06:46:21 ; Search time 8843 Seconds  
 (without alignments)  
 11454.565 Million cell updates/sec

Title: US-10-765-456-3

Perfect score: 1584

Sequence: 1 atgaaatcaaactctaaaa.....tcagggtataatggatgg 1584

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
 Listing first 45 summaries

Database : GenBank:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb\_D1:\*

5: gb\_pr:\*

6: gb\_rn:\*

7: gb\_stb:\*

8: gb\_sy:\*

9: gb\_uni:\*

10: gb\_vl:\*

11: gb\_ov:\*

12: gb\_htg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	1564.8	98.8	1905	AF124843 Fusarium Locus AF124843
2	1543.4	97.9	1726	AF05241 Fusarium Locus AF05241
3	1185.6	74.8	1836	AF124844 Fusarium Locus AF124844
4	68.2	4.3	7218	16694 Sequence 14 AF05240 Fusarium AF05240
5	64.4	4.1	785	AF05240 Fusarium AF05240
6	50.8	3.2	2000	AFX55393 Sequence source
7	48.4	3.1	14461	2 AX26438 Sequence source
8	48.2	3.0	2000	2 AX55393 Sequence source
9	46.2	2.9	335050	13 PPA929356 Sequence AL929356 Iasmidu AC023358 Homo sapi AC027784 Homo sapi AC018927 Homo sapi AC010675 Sequence AC010675 Arabidops AC02062 Sequence AL772262 Human DNA AB169417 Macaca fasciata AL929043 Mouse DNA
10	45.8	2.9	104492	12 AC027784 Homo sapi AC018927 Homo sapi AC050875 Sequence AC010675 Arabidops AC02062 Sequence AL772262 Human DNA AB169417 Macaca fasciata AL929043 Mouse DNA
11	45.8	2.9	157097	12 AC027784 Homo sapi AC018927 Homo sapi AC050875 Sequence AC010675 Arabidops AC02062 Sequence AL772262 Human DNA AB169417 Macaca fasciata AL929043 Mouse DNA
12	45.8	2.9	184864	5 AC010927 Sequence source
13	45.4	2.9	2000	2 AX50875 Sequence source
14	45.4	2.9	84723	4 AC010675 Sequence source
15	45.4	2.9	114505	4 F20P5 Sequence source
16	44.8	2.8	147079	5 AL772262 Sequence source
17	44.6	2.8	2822	5 AB169417 Macaca fasciata
18	44.6	2.8	164834	6 AL929043 Mouse DNA

**ALIGNMENTS**

RESULT 1

AF124843 Locus AF124843 Fusarium oxyasperum f. sp. raphani mitochondrial plasmid PLN 02-JUL-2003 DEFINITION 1905 bp DNA linear complete sequence.

ACCESSION AF124843

VERSION AF124843.1 GI:5052123

KEYWORDS

SOURCE

ORGANISM Fusarium oxyasperum f. sp. raphani

Bakteria; Fungi; Ascomycota; Pezizomycotina; Sordariomycetidae; Hypocreales; Fusarium; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxyasperum complex.

REFERENCE 1 (bases 1 to 1905)

AUTHORS Walther, T.C. and Keneil, J.C.

TITLE Linear mitochondrial plasmids of *F. oxyasperum* are novel, telomere-like retroelements

JOURNAL Mol. Cell. 4 (2), 229-238 (1999)

REFERENCE 2 (bases 1 to 1905)

AUTHORS Keneil, J.C. and Walther, T.C.

JOURNAL Submitted (30-JUN-1999) Biological Sciences, Southern Methodist University, 220 Founders Science, Dallas, TX 75275-0376, USA

FEATURES

source

1..1905

/organism="Fusarium oxyasperum f. sp. raphani"  
 /mol\_type="genomic DNA"  
 /strain="659"  
 /db\_xref="taxon:96118"  
 /plasmid="PROXC2"  
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 /cdon\_end=1855  
 /transl\_table=4  
 /product="reverse transcriptase"  
 /protein\_id="RND385033.1"  
 /db\_xref="IGI:02334"  
 /translation="MNOQISRNDSLVDQDEMGGKTFESRKSLSGMDYFKSLSGIR

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GenCore version 5.1.9

Om nucleic - nucleic search, using BW model  
Run on: July 11, 2006, 06:46:35 ; Search time 7954 Seconds  
(without alignments)  
11136.060 Million cell updates/sec

Title: US-10-765-456-3

Perfect score: 1584  
Sequence: 1 atgaatccaaatctctaaaa.....tcagggtataatttagtag 1584

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 BEGB, 27959655780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

#### Database :

- EST:\*
- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est7:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	87.6	5.5	281	DW177370
2	57.6	3.6	997	CNS005TE
3	50.8	3.2	1687	AM090701
4	50.4	3.2	1101	CNS0039G
5	49.8	3.1	1101	CNS012VN
6	47.2	3.0	1050	AGI13232
7	47.2	3.0	1101	CNS006J
8	47.0	3.0	956	CT070073
9	47.0	3.0	1007	CNS00JOV
10	46.0	2.9	1101	CNS0106X
11	45.8	2.9	1101	CNS011TX
12	45.4	2.9	1101	CNS000DI
13	44.8	2.8	684	BA2433974
14	44.8	2.8	777	BZ071235
15	44.8	2.8	786	BH938760
16	44.8	2.8	1342	DV781885
17	44.4	2.8	742	AG469000
18	44.4	2.8	839	DUS95126
19	44.4	2.8	1204	CNS016B2

#### ALIGNMENTS

RESULT 1  
DW177370  
LOCUS DW177370 281 bp mRNA linear EST 29-BBC-2005  
DEFINITION Fusarium culmorum Differential Display library  
Fusarium culmorum cDNA, mRNA sequence.  
ACCESSION DW177370  
VERSION DW177370.1 GI:84067500  
KEYWORDS EST  
SOURCE Fusarium culmorum  
ORGANISM Fusarium culmorum  
Bakteria; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
REFERENCE 1  
LYSOE, E., BONE, K. and KLEMSDAL, S.  
AUTHORS  
TITLE Differential Display RT-PCR in high zearylone producing strains  
of Fusarium  
JOURNAL Unpublished (2005)  
COMMENT Contact: Lysoe E  
Bioforsk Plantehelse  
Genetics and biotechnology  
Hogskoleveien 7, 1432 Aas, Norway  
Email: erik.lysoe@bioforsk.no.  
Tel: +47 69949252  
Fax: +47 64947110  
FEATURES  
source  
1. Location/Qualifiers  
/organism="Fusarium culmorum"  
/mol\_type="mRNA"  
/db\_xref="taxon:5516"  
/clone\_lib="Fusarium culmorum Differential Display library"  
ORIGIN  
Query Match Similarity 5.5%; Score 87.6; DB 10; Length 281;  
Best Local Similarity 5.72%; Pred. No. 4.1e-12;  
Matches 159; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
QY 151 GGATGTGATTAGAGAGTCAGAAGCAATAGATACTGCCTCCAGGCAAGG 210  
2 GGGATTAAGTACTCTGAGCTAGACAGGCCATAGGTTCTACATTCAGGAGTGAGA 61  
Db QY 211 ATTGTTAGCGCAATAGAAGGCCGGAATTCTGAAGGGCAGTGTGGCTATGTTA 270

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## OM nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:44:56 ; Search time 967 Seconds

(without alignments)  
11420.932 Million cell updates/sec

Title: US-10-765-456-3

Perfect score: 1584

Sequence: 1 atgatccaatctctaaaa.....tcagggtataattggtag 1584

## Scoring table: IDENTITY\_NUC

GapOp 10.0 , GapExt 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:

10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

N\_Geneseq\_8:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

## ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	19	38.2	2.4	156652	AEG61138 Human UGT
C	20	38	2.4	114633	ACM44332 Mouse gen
C	21	37.8	2.4	1395	AAS71385 DNA encod
C	22	37.8	2.4	3540	Aax05875 Yeast NPC
C	23	37.8	2.4	6815	AAS1927
C	24	37.8	2.4	6815	AAS35101
C	25	37.8	2.4	6815	ADC46543
C	26	37.6	2.4	324	ABL7477
C	27	37.6	2.4	90183	ADQ97950_3
C	28	37.6	2.4	95124	AER04750
C	29	37.4	2.4	544	AX20395
C	30	37.4	2.4	678	ADM91226
C	31	37.4	2.4	678	ADM90808
C	32	37.4	2.4	678	ADM90807
C	33	37.4	2.4	678	ADM91225
C	34	37.4	2.4	9370	ABU10890
C	35	37.2	2.3	94330	ACN44662
C	36	37	2.3	517	ABE60603
C	37	37	2.3	517	AAI40491
C	38	37	2.3	517	AKX0885
C	39	37	2.3	922	ABZ17364
C	40	37	2.3	6741	AAA10595
C	41	36.8	2.3	5032	AAS94838
C	42	36.8	2.3	5032	AD161646
C	43	36.8	2.3	5032	AAI43811
C	44	36.8	2.3	177856	ADL13935
C	45	36.6	2.3	2000	ABZ15784

X	X	X	X	X	X
X	X	X	X	X	X
X	X	X	X	X	X
X	X	X	X	X	X
X	X	X	X	X	X

PN	US2004157213-A1.	XX	XX	XX	XX
PD	12-AUG-2004.	XX	XX	XX	XX
PF	26-JAN-2004; 20044US-00765456.	XX	XX	XX	XX
PR	27-JAN-2003; 2003US-04428855P.	XX	XX	XX	XX
PR	02-APR-2003; 2003US-04597755P.	XX	XX	XX	XX
PA	(KENN/ ) KENNELL J C.	XX	XX	XX	XX
PT	Kennell JC;	XX	XX	XX	XX
PT	WRI; 2004-580263/56.	XX	XX	XX	XX
PT	P-PSDB; ADR14865.	XX	XX	XX	XX
PT	New isolated fungal reverse transcriptases with enhanced capabilities, and encoding nucleic acid molecules, useful for research and diagnostic applications.	XX	XX	XX	XX

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On nucleic - nucleic search, using sw model

Run on: July 11, 2006, 06:49:55 ; Search time: 1862 Seconds  
(without alignment)

14153.069 Million cell updates/sec

Title: US-10-765-456-3  
Perfect score: 1584  
Sequence: ATGAAATCAATCTCAAATAATGACACTTAGTGTCTTCAGGATGAATGGACAAA  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listning first 45 summaries

Database : Published Applications NA Main:  
 1: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us07\_PUBCOMB.seq: \*  
 2: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us07\_PUBCOMB.seq: \*  
 3: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us09\_PUBCOMB.seq: \*  
 4: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us09\_PUBCOMB.seq: \*  
 5: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us09C\_PUBCOMB.seq: \*  
 6: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10\_PUBCOMB.seq: \*  
 7: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10\_PUBCOMB.seq: \*  
 8: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10C\_PUBCOMB.seq: \*  
 9: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10E\_PUBCOMB.seq: \*  
 10: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10F\_PUBCOMB.seq: \*  
 11: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us10G\_PUBCOMB.seq: \*  
 12: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us11A\_PUBCOMB.seq: \*  
 13: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us11B\_PUBCOMB.seq: \*  
 14: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us11C\_PUBCOMB.seq: \*  
 15: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us11D\_PUBCOMB.seq: \*  
 16: /EMC\_Celerra\_SIDS3/prodata/2/pubpna/us11D\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	1584	100.0	1584	Sequence 3, Appli
2	1564.8	98.8	1905	Sequence 5, Appli
3	1204.8	76.1	1584	Sequence 4, Appli
4	1185.6	74.8	1836	Sequence 6, Appli
5	45.4	2.9	2000	Sequence 3270, Ap
6	45.4	2.9	2000	Sequence 3270, Ap
7	42.8	2.7	1230	Sequence 281, Ap
8	42.8	2.7	1330	Sequence 5516, Ap
9	42.2	2.7	660	Sequence 480, Ap
10	42.2	2.7	660	Sequence 480, Ap
11	42.2	2.7	660	Sequence 480, Ap
12	42.2	2.7	660	Sequence 480, Ap
13	42.2	2.7	660	Sequence 480, Ap
14	42.2	2.7	660	Sequence 480, Ap
15	42.2	2.7	660	Sequence 480, Ap
16	42.2	2.7	660	Sequence 480, Ap
17	42.2	2.7	660	Sequence 480, Ap

**ALIGNMENTS**

US-10-765-456-3

RESULT 1

; Sequence 3, Application US/10765456  
; Publication No. US20040157213A1  
; GENERAL INFORMATION:  
; APPLICANT: Kennell, John C.  
; TITLE OF INVENTION: Fungal Reverse Transcriptases with Enhanced Capabilities  
; FILE REFERENCE: SU02-010  
; CURRENT APPLICATION NUMBER: US/10/765,456  
; CURRENT FILING DATE: 2004-01-26  
; PRIORITY APPLICATION NUMBER: 60/442,885  
; PRIORITY FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Microsoft Word 2000  
; SEQ ID NO: 3  
; LENGTH: 1584  
; TYPE: DNA  
; ORGANISM: fungal

US-10-765-456-3

Query Match Score: 100.0%; Score: 1584; DB: 8; Length: 1584;  
Best Local Similarity: 100.0%; Pred. No.: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
Matches 1584; Conservative: 0;

Qy	1	ATGAAATCAATCTCAAATAATGACACTTAGTGTCTTCAGGATGAATGGACAAA	60
Db	1	ATGAAATCAATCTCAAATAATGACACTTAGTGTCTTCAGGATGAATGGACAAA	60
Qy	61	AAGACCTTGAGTCAGAAAGAACTCTCTAGTGGATTACTTCATCGCTAGGAAATGGACAAA	60
Db	61	AAGACCTTGAGTCAGAAAGAACTCTCTAGTGGATTACTTCATCGCTAGGAAATGGACAAA	60
Qy	61	AAGACCTTGAGTCAGAAAGAACTCTCTAGTGGATTACTTCATCGCTAGGAAATGGACAAA	60
Db	61	AAGACCTTGAGTCAGAAAGAACTCTCTAGTGGATTACTTCATCGCTAGGAAATGGACAAA	60
Qy	121	AGTATGGTAGTTACACATTTCAGGAGGAATGAGGATGTTGCGCATGAGCCGGGAATT	120
Db	121	AGTATGGTAGTTACACATTTCAGGAGGAATGAGGATGTTGCGCATGAGCCGGGAATT	120
Qy	181	ATAGATATCTGCCCTCCAGGAGCAAGGATGTTGCGCATGAGCCGGGAATT	120
Db	181	ATAGATATCTGCCCTCCAGGAGCAAGGATGTTGCGCATGAGCCGGGAATT	120

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OM nucleic - nucleic search, using sw model.  
Run on: July 11, 2006, 06:47:12 ; Search time 320 Seconds  
(without alignments)

9261.989 Million cell updates/sec

Title: US-10-765-456-3  
Perfect score: 1584  
Sequence: 1 atgaatcaaactctaaaa.....tcagggctataattgagtag 1584  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:

2807332

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/5\_COMB.seq:\*

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5: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/H\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/PCTUS\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/PP\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/RB\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/backfileseq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/in/a/backfileseq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
C 1	68.2	4.3	7218	2 US-08-232-463-14	Sequence 14, Appl
C 2	40.6	2.6	1141	3 US-09-806-708B-22	Sequence 22, Appl
C 3	39.6	2.5	818128	3 US-09-949-016-14546	Sequence 14546, A
C 4	39.5	2.5	818128	3 US-09-949-016-14547	Sequence 14547, A
C 5	39.6	2.5	818128	3 US-09-949-016-15458	Sequence 14548, A
C 6	39.6	2.5	818128	3 US-09-949-016-15459	Sequence 14549, A
C 7	39.6	2.5	818128	3 US-09-949-016-15500	Sequence 14550, A
C 8	39.6	2.5	818128	3 US-09-949-016-1551	Sequence 14551, A
C 9	39.6	2.5	818128	3 US-09-949-016-14552	Sequence 14552, A
C 10	39.6	2.5	818128	3 US-09-949-016-14553	Sequence 14553, A
C 11	39.6	2.5	818128	3 US-09-949-016-14554	Sequence 14554, A
C 12	39.6	2.5	818128	3 US-09-949-016-14555	Sequence 14555, A
C 13	39.6	2.5	818128	3 US-09-949-016-14561	Sequence 14556, A
C 14	39.6	2.5	818128	3 US-09-949-016-14557	Sequence 14557, A
C 15	39.6	2.5	818128	3 US-09-949-016-14558	Sequence 14558, A
C 16	39.6	2.5	818128	3 US-09-949-016-14559	Sequence 14559, A
C 17	39.6	2.5	818128	3 US-09-949-016-14560	Sequence 14560, A
C 18	39.6	2.5	818128	3 US-09-949-016-14561	Sequence 14561, A
C 19	39.6	2.5	818128	3 US-09-949-016-14562	Sequence 14562, A
C 20	39.6	2.5	818128	3 US-09-949-016-14564	Sequence 14563, A
C 21	39.6	2.5	818128	3 US-09-949-016-14565	Sequence 14565, A
C 22	39.6	2.5	818128	3 US-09-949-016-14566	Sequence 14566, A
C 23	39.6	2.5	818128	3 US-09-949-016-14567	Sequence 14567, A

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Hardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER: COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE: 12-12-1991  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE: 07-12-1991  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 856-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDBEADNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:

Sequence 12228, A  
Sequence 12240, A  
Sequence 22, Appl  
Sequence 5, Appl  
Sequence 16528, A  
Sequence 14389, A  
Sequence 13104, A  
Sequence 32792, A  
Sequence 32851, A  
Sequence 50709, A  
Sequence 50768, A  
Sequence 12508, A  
Sequence 13211, A  
Sequence 13212, A  
Sequence 12509, A  
Sequence 15770, A  
Sequence 5435, Ap  
Sequence 14, Appl  
Sequence 1378, A  
Sequence 12455, A  
Sequence 13905, A  
Sequence 13906, A